



# results of **BLAST**

## **BLASTP 2.2.7 [Dec 30 2003]**

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1072811300-17465-209900690670.BLASTQ4

### **Query=**

(471 letters)

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,585,607 sequences; 519,349,222 total letters

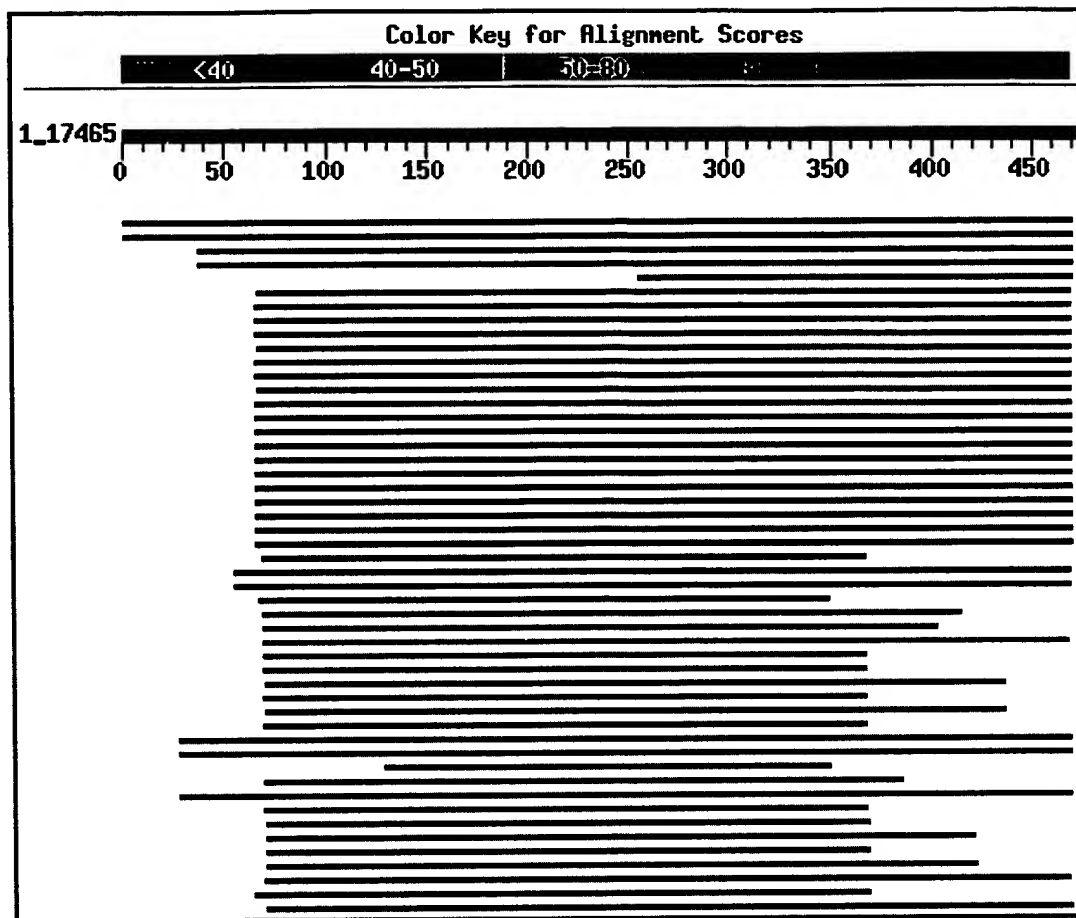
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## **Distribution of 50 Blast Hits on the Query Sequence**

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Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score	E
(bits)	Value

<a href="#">gi 32699007 ref NP_872395.1 </a>	5-hydroxytryptamine serotonin ...	<a href="#">954</a>	0.0	<b>L</b>
<a href="#">gi 37574914 qb AAQ93477.1 </a>	5-HT3cl serotonin receptor-like ...	<a href="#">924</a>	0.0	<b>L</b>
<a href="#">gi 38146010 ref NP_938055.1 </a>	5-hydroxytryptamine serotonin ...	<a href="#">854</a>	0.0	<b>L</b>
<a href="#">gi 18640740 ref NP_570126.1 </a>	5-hydroxytryptamine receptor 3...	<a href="#">681</a>	0.0	<b>L</b>
<a href="#">gi 32698904 ref NP_872343.1 </a>	5-hydroxytryptamine receptor 3...	<a href="#">367</a>	e-100	<b>L</b>
<a href="#">gi 9790622 qb AAB37533.2 </a>	5-hydroxytryptamine type 3AS rece...	<a href="#">291</a>	2e-77	<b>L</b>
<a href="#">gi 30583247 qb AAP35868.1 </a>	5-hydroxytryptamine (serotonin) ...	<a href="#">291</a>	3e-77	<b>L</b>
<a href="#">gi 4504543 ref NP_000860.1 </a>	5-hydroxytryptamine (serotonin)...	<a href="#">291</a>	3e-77	<b>L</b>
<a href="#">gi 30585371 qb AAP36958.1 </a>	Homo sapiens 5-hydroxytryptamine...	<a href="#">291</a>	3e-77	
<a href="#">gi 1586341 prf  2203408A</a>	serotonin 3AS receptor	<a href="#">290</a>	5e-77	
<a href="#">gi 2978508 qb AAC06137.1 </a>	5-HT3-As receptor precursor [Cavi...	<a href="#">287</a>	3e-76	
<a href="#">gi 13242306 ref NP_077370.1 </a>	5-hydroxytryptamine (serotonin...	<a href="#">285</a>	9e-76	<b>L</b>
<a href="#">gi 8247752 dbj BAA96417.1 </a>	ferret 5-HT3A receptor [Mustela ...	<a href="#">285</a>	1e-75	
<a href="#">gi 1168223 sp P35563 5HT3_RAT</a>	5-hydroxytryptamine 3 recepto...	<a href="#">284</a>	2e-75	<b>L</b>
<a href="#">gi 2144046 pir  I58179</a>	5HT3 receptor subunit - rat (fragmen...	<a href="#">283</a>	4e-75	
<a href="#">gi 488695 emb CAA55871.1 </a>	5HT3 receptor [Mus musculus]	<a href="#">283</a>	5e-75	<b>L</b>
<a href="#">gi 24211440 sp O70212 5HT3_CAVPO</a>	5-hydroxytryptamine 3 rece...	<a href="#">283</a>	7e-75	
<a href="#">gi 7305175 ref NP_038589.1 </a>	5-hydroxytryptamine (serotonin)...	<a href="#">282</a>	1e-74	<b>L</b>
<a href="#">gi 543183 pir  S41757</a>	5-hydroxytryptamine-3 receptor - mouse	<a href="#">281</a>	2e-74	

gi 488694 emb CAA55870.1	5HT3 receptor [Mus musculus]	281	2e-74	L
gi 21314591 gb AAM47014.1	5-hydroxytryptamine receptor 3A ...	281	2e-74	L
gi 313864 emb CAA51089.1	5-hydroxytryptamine3 receptor [Mu...	280	3e-74	L
gi 817940 emb CAA80453.1	5HT3 receptor [Mus musculus]	279	7e-74	L
gi 3115222 emb CAA05851.1	serotonin receptor [Homo sapiens]	274	3e-72	L
gi 28277272 gb AAH44101.1	MGC52789 protein [Xenopus laevis]	213	5e-54	L
gi 9938026 ref NP_064670.1	5-hydroxytryptamine (serotonin)...	213	8e-54	L
gi 11559956 ref NP_071525.1	5-hydroxytryptamine (serotonin)...	212	1e-53	L
gi 5174469 ref NP_006019.1	5-hydroxytryptamine (serotonin)...	206	8e-52	L
gi 31790123 gb AAP58387.1	nicotinic acetylcholine receptor...	176	6e-43	
gi 31790121 gb AAP58386.1	nicotinic acetylcholine receptor...	173	6e-42	
gi 7407125 gb AAF61920.1	nicotinic acetylcholine receptor ...	171	3e-41	L
gi 9501306 emb CAB99482.1	alpha 10 subunit of nicotinic ac...	171	3e-41	
gi 8923742 ref NP_060051.1	cholinergic receptor, nicotinic...	171	4e-41	L
gi 5777609 emb CAB53472.1	nicotinic acetylcholine receptor...	170	4e-41	L
gi 38081753 ref XP_132045.2	cholinergic receptor, nicotini...	170	6e-41	L
gi 31542395 ref NP_067344.2	cholinergic receptor, nicotini...	170	7e-41	L
gi 31790117 gb AAP58384.1	nicotinic acetylcholine receptor...	169	1e-40	
gi 27532980 ref NP_775304.1	cholinergic receptor, nicotini...	168	2e-40	L
gi 18542399 gb AAL75573.1	nicotinic acetylcholine receptor...	168	2e-40	L
gi 11120504 gb AAG30903.1	5-hydroxytryptamine 3 receptor B...	168	2e-40	L
gi 6692362 gb AAF24618.1	neuronal acetylcholine receptor s...	167	4e-40	
gi 19424304 ref NP_598281.1	cholinergic receptor, nicotini...	167	6e-40	L
gi 12621088 ref NP_075219.1	acetylcholine receptor alpha 9...	166	9e-40	L
gi 31745832 gb AAP57217.1	nicotinic acetylcholine receptor...	166	1e-39	
gi 17105332 ref NP_476532.1	cholinergic receptor, nicotini...	165	2e-39	L
gi 34878975 ref XP_346491.1	hypothetical protein XP_346490...	164	3e-39	L
gi 34148146 gb AAQ62631.1	nicotinic acetylcholine receptor...	164	3e-39	
gi 11138123 ref NP_065135.2	cholinergic receptor, nicotini...	163	5e-39	L
gi 31745830 gb AAP57216.1	nicotinic acetylcholine receptor...	162	9e-39	
gi 104800 pir B39218	nicotinic acetylcholine receptor alph...	162	9e-39	

## Alignments

Get selected sequences Select all Deselect all

>gi|32699007|ref|NP\_872395.1| L 5-hydroxytryptamine serotonin receptor 3E [Homo  
gi|31790914|gb|AAO38167.1| L 5-hydroxytryptamine serotonin receptor 3E [Homo sapi  
Length = 471

Score = 954 bits (2467), Expect = 0.0

Identities = 467/471 (99%), Positives = 469/471 (99%)

Query: 1 MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTAV 60  
MLAFILSRATPRPALGPLSYRE RVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTA+  
Sbjct: 1 MLAFILSRATPRPALGPLSYRERRVALLHLTHSMSTTGRGVFTFTINCSGFGQHGDPTAL 60

Query: 61 NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE 120  
NSVFNRKPFPRPVTNISV TQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE

Sbjct: 61 NSVFNRKPFPRPVTNISVLTVQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE 120

Query: 121 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 180  
ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD

Sbjct: 121 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 180

Query: 181 IFYFPFDQQNCTLTFFSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 240  
IFYFPFDQQNCTLTFFSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA

Sbjct: 181 IFYFPFDQQNCTLTFFSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 240

Query: 241 KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 300  
KLSRGGNLYD+IVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL

Sbjct: 241 KLSRGGNLYDRIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 300

Query: 301 LLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360  
LLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR

Sbjct: 301 LLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360

Query: 361 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE 420  
WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE

Sbjct: 361 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE 420

Query: 421 WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 471  
WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT

Sbjct: 421 WTRAQREHEAQKQHSVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 471

[gi|37574914|gb|AA093477.1|](#) **L** 5-HT3c1 serotonin receptor-like protein [Homo sapi  
Length = 456

Score = 924 bits (2387), Expect = 0.0

Identities = 455/471 (96%), Positives = 456/471 (96%), Gaps = 15/471 (3%)

Query: 1 MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTTINCSGFGQHGDPTAV 60  
MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTTINCSGFGQHGDPTA+

Sbjct: 1 MLAFILSRATPRPALGPLSYREHRVALLHLTHSMSTTGRGVFTTINCSGFGQHGDPTAL 60

Query: 61 NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPE 120  
NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDV VWDNPFISWNPE

Sbjct: 61 NSVFNRKPFPRPVTNISVPTQVNISFAMSAILDV-----VWDNPFISWNPE 105

Query: 121 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 180  
ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD

Sbjct: 106 ECEGITKMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLD 165

Query: 181 IFYFPFDQQNCTLTFFSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 240  
IFYFPFDQQNCTLTFFSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA

Sbjct: 166 IFYFPFDQQNCTLTFFSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATA 225

Query: 241 KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 300  
KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL

Sbjct: 226 KLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITL 285

Query: 301 LLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360  
LLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR

Sbjct: 286 LLGYNVFLLMMSDLLPTSGTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 345

Query: 361 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE 420  
WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGGSE

Sbjct: 346 WLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAAEALTGGSE 405

Query: 421 WTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLFMASSIITVICLWNT 471

WTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLFMASSIITVICLWNT

Sbjct: 406 WTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLFMASSIITVICLWNT 456

[gi|38146010|ref|NP\\_938055.1|](#) **L** 5-hydroxytryptamine serotonin receptor 3E [Homo  
[gi|37574912|gb|AAQ93476.1|](#) **L** 5-HT3c1 serotonin receptor-like protein [Homo sapien  
 Length = 441

Score = 854 bits (2206), Expect = 0.0

Identities = 418/434 (96%), Positives = 419/434 (96%), Gaps = 15/434 (3%)

Query: 38 GRGVTFTINCSGFGQHGDPTAVNSVFNRKPFPRVTNISVPTQVNISFAMSAILDVNEQL 97

GRGVTFTINCSGFGQHGDPTA+NSVFNRKPFPRVTNISVPTQVNISFAMSAILDV

Sbjct: 23 GRGVTFTINCSGFGQHGDPTALNSVFNRKPFPRVTNISVPTQVNISFAMSAILDV---- 78

Query: 98 HLLSSFLWLEMVWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIELMVDVDPKGLTA 157

VWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIELMVDVDPKGLTA

Sbjct: 79 -----VWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIELMVDVDPKGLTA 127

Query: 158 YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDMSLLDMEKEVWEIT 217

YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDMSLLDMEKEVWEIT

Sbjct: 128 YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDMSLLDMEKEVWEIT 187

Query: 218 DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV 277

DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV

Sbjct: 188 DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV 247

Query: 278 AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS 337

AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS

Sbjct: 248 AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS 307

Query: 338 LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV 397

LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV

Sbjct: 308 LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV 367

Query: 398 KEPEVSAGQMPGPAAEALTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLF 457

KEPEVSAGQMPGPAAEALTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLF

Sbjct: 368 KEPEVSAGQMPGPAAEALTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLF 427

Query: 458 MASSIITVICLWNT 471

MASSIITVICLWNT

Sbjct: 428 MASSIITVICLWNT 441

[gi|18640740|ref|NP\\_570126.1|](#) **L** 5-hydroxytryptamine receptor 3 subunit C [Homo :  
[gi|18251966|gb|AAL66182.1|](#) **L** 5-hydroxytryptamine receptor 3 subunit C [Homo sapie  
 Length = 447

Score = 681 bits (1756), Expect = 0.0

Identities = 327/434 (75%), Positives = 368/434 (84%), Gaps = 9/434 (2%)

Query: 38 GRGVTFTINCSGFGQHGDPTAVNSVFNRKPFPRVTNISVPTQVNISFAMSAILDVNEQL 97

GRG FTINCSGF QHG DP +VF+RK FRP TN S+PT+VNISF +SAIL V+ QL

Sbjct: 23 GRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNYSIPTRVNISFTLSAILGVDAQL 82

Query: 98 HLLSSFLWLEMVWDNPFISWNPEECEGITKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTA 157  
 LL+SFLW+++VWDNPF+WNPE+EC GI K+++ A+NLWLPDIFI+E MDVD+TP GLTA  
 Sbjct: 83 QLLTSFLWMDLVWDNPFINWNPKCECVGINKLTVLAENLWLPDIFIVESMDVDQTPSGLTA 142

Query: 158 YVSNEGRIRYKKPMKVDSICNLDFYFPFDQQNCTLTFSFLYTVDSMLLDMEKEVWEIT 217  
 Y+S+EGRI+Y KPM+V SIC LDIFYFPFDQQNCT TFSSFLYTVDSMLL M+KEVWEIT  
 Sbjct: 143 YISSEGRIKYDKPMRVTSICKLDIFYFPFDQQNCTFTFSFLYTVDSMLLGMDKEVWEIT 202

Query: 218 DASRNILQTHGEWELLGLSKATAKLSRGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLV 277  
 D SR ++QT GEWELLG++KAT K+S G NLYDQI+FYVAIRRRPSLY+INLLVPS FLV  
 Sbjct: 203 DTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFYVAIRRRPSLYIINLLVPSFLV 262

Query: 278 AIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSDLLPTSGTPLIGVYFALCLSLMVGS 337  
 AIDALSFYLP +S NR PFKITLLLGYNVFLMMDLLP SGTPLI VYFALCLSLMV S  
 Sbjct: 263 AIDALSFYLPAESENRAFPFKITLLLGYNVFLMMDLLPASGTPLISVYFALCLSLMVVS 322

Query: 338 LLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGV 397  
 LLET+FIT+LLHVATTQPPP+PRWLHSLLLHC SPGRCCPTAPQK NKG GLT THLPG  
 Sbjct: 323 LLETVFITYLLHVATTQPPMPRWLHSLLLHCTSPGRCCPTAPQKGNKGLGLTLTHLPGP 382

Query: 398 KEPEVSAGQMPGPAEAEELTGGSEWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLF 457  
 KEP AG+ GP E E GGS WT+ Q +ELW+QFSHMD +LFRLYLLF  
 Sbjct: 383 KEPGELAGKKLGPTEPEDGGSAAWTKTQL-----MELWVQFSHAMDTLLFRLYLLF 433

Query: 458 MASSIITVICLWNT 471  
 MASSI+TVI LWNT  
 Sbjct: 434 MASSILTVIVLWNT 447

□ >gi|32698904|ref|NP\_872343.1| **L** 5-hydroxytryptamine receptor 3 subunit D; similar  
 5-hydroxytryptamine receptor 3 subunit C [Homo sapiens]  
 gi|31790912|gb|AA038166.1| **L** 5-hydroxytryptamine serotonin receptor 3D [Homo sapiens]  
 Length = 279

Score = 367 bits (943), Expect = e-100

Identities = 188/232 (81%), Positives = 200/232 (86%), Gaps = 16/232 (6%)

Query: 256 VAIRRR--PSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLLGYNVFLMMSD 313  
 VAIR R PS YV+N LVPSG L+AIDALSFYLP +SGN PFK+T+LLGY+VFLMMD  
 Sbjct: 48 VAIRHRCRSPYVNVFLVPSGILIAIDALSFYLPPESGNCAPFKMTVLLGYSVFLMMD 107

Query: 314 LLPTSGTP----LI-----GVYFALCLSLMVGSLLLETIFITHLLHVATTQPPPLP 359  
 LLP + T L+ GVYFALCLSLMVGSLLLETIFITHLLHVATTQPP PLP  
 Sbjct: 108 LLPATSTSSHASLVRPHPSRDQKRGVYFALCLSLMVGSLLLETIFITHLLHVATTQPLPLP 167

Query: 360 RWLHSLLLHCNSPGRCCPTAPQKENKGPGLTPTHLPGVKEPEVSAGQMPGPAEAEELTGG 419  
 RWLHSLLLHC GRCCPTAPQK NKGPG+TPTHLPGVKEPEVSAGQMPGP EAEELTGG  
 Sbjct: 168 RWLHSLLLHCTGQGRCCPTAPQKGNKGPVTPPTHLPGVKEPEVSAGQMPGPAEAEELTGG 227

Query: 420 EWTRAQREHEAQKQHSVELWLQFSHAMDLFRLYLLFMMASSIITVICLWNT 471  
 EWTRAQREHEAQKQHSVELW+QFSHAMDA+LFRLYLLFMMASSIITVICLWNT  
 Sbjct: 228 EWTRAQREHEAQKQHSVELWVQFSHAMDALLFRLYLLFMMASSIITVICLWNT 279

□ >gi|9790622|gb|AAB37533.2| **L** 5-hydroxytryptamine type 3AS receptor subunit [Homo sapiens]  
 Length = 478

Score = 291 bits (745), Expect = 2e-77

Identities = 170/432 (39%), Positives = 254/432 (58%), Gaps = 33/432 (7%)

Query: 67 KPFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGIT 126  
 K RPV + PT V+I + AIL+V+E+ +L+++W W + F+ WNPE+ + IT  
 Sbjct: 47 KGVPRPVRDWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNIT 106

Query: 127 KMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFPF 186  
 K+S+ ++W+PDI I EL+DV K+P Y+ ++G ++ KP++V + C+LDI+ FPF  
 Sbjct: 107 KLSIPTDSIWVPDILINELVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFPF 166

Query: 187 DQQNCTLTFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKLS 243  
 D QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ + S  
 Sbjct: 167 DVQNCSLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREFS 222



Query: 244 -RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLL 302  
 N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLLL  
 Sbjct: 223 MESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNNGERSVSFKITLLL 282

Query: 303 GYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPR 360  
 GY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P  
 Sbjct: 283 GYSVFLIIVSDTLPTAIGTPLIGVYFVVMALLVISLTETIFIVRLVHKQDLQ-QPVPA 341

Query: 361 WLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEVS 403  
 WL L+L + C P A + K G TH+ G K P  
 Sbjct: 342 WLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCTHMGGPQDFEKS PRDR 401

Query: 404 AGQMPGPAEAELT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLFM 458  
 P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL +  
 Sbjct: 402 CSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLAV 461

Query: 459 ASSIITVICLWN 470  
 + IT++ LW+  
 Sbjct: 462 LAYSITLVMLWS 473

 >gi|30583247|gb|AAP35868.1|  5-hydroxytryptamine (serotonin) receptor 3A [Homo  
 Length = 484

Score = 291 bits (744), Expect = 3e-77

Identities = 169/433 (39%), Positives = 254/433 (58%), Gaps = 33/433 (7%)

Query: 66 RKPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGI 125  
 RK RPV + PT V+I + AIL+V+E+ +L+++W W + F+ WNPE+ + I  
 Sbjct: 52 RKGVRPVRDWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNI 111

Query: 126 TKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFP 185  
 TK+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FP  
 Sbjct: 112 TKLSIPTDSIWVPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFP 171

Query: 186 FDQQNCTLTFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKL 242  
 FD QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ +  
 Sbjct: 172 FDVQNCSLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREF 227

Query: 243 S-RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 301  
 S N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLL  
 Sbjct: 228 SMESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNNGERSVSFKITLL 287

Query: 302 LGYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLP 359  
 LGY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P  
 Sbjct: 288 LGYSVFLIIVSDTLPATAIGTPLIGVYFVVCMLLVISLAETIFIVRLVHKQDLQ-QPVP 346

Query: 360 RWLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEV 402  
 WL L+L + C P A + K G +H+ G K P  
 Sbjct: 347 AWLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGGPQDFEKS PRD 406

Query: 403 SAGQMPGPAAEALT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMFLRLYLLF 457  
 P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL  
 Sbjct: 407 RCSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLA 466

Query: 458 MASSIITVICLWN 470  
 + + IT++ LW+  
 Sbjct: 467 VLAYSITLVMLWS 479

└>gi|4504543|ref|NP\_000860.1| **L** 5-hydroxytryptamine (serotonin) receptor 3A; 5-HT  
 5-hydroxytryptamine (serotonin) receptor-3 [Homo  
 sapiens]

gi|1168222|sp|P46098|5HT3\_HUMAN **L** 5-hydroxytryptamine 3 receptor precursor (5-HT-  
 ion channel receptor) (5-HT3R)

gi|681914|dbj|BAA08387.1| **L** serotonin 5-HT3 receptor [Homo sapiens]

gi|3115224|emb|CAA05852.1| **L** 5-hydroxytryptamine3 receptor [Homo sapiens]

gi|9715820|emb|CAA06442.3| serotonin 3 receptor [Homo sapiens]

gi|12803101|gb|AAH02354.1| **L** 5-hydroxytryptamine (serotonin) receptor 3A [Homo sa]

gi|20379142|gb|AAM21131.1| **L** 5-hydroxytryptamine receptor 3A [Homo sapiens]

gi|37514834|gb|AAH04453.2| **L** 5-hydroxytryptamine (serotonin) receptor 3A [Homo sa]  
 Length = 478

Score = 291 bits (744), Expect = 3e-77

Identities = 169/433 (39%), Positives = 254/433 (58%), Gaps = 33/433 (7%)

Query: 66 RKPFRPVNTNISVPTQVNISFAMSAILDVNEQLHLSSFLWLEMVWDNPFISWNPEECEGI 125  
 RK RPV + PT V+I + AIL+V+E+ +L+++W W + F+ WNPE+ + I  
 Sbjct: 46 RKGVRPVRDWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNI 105

Query: 126 TKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDFYFP 185  
 TK+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FP  
 Sbjct: 106 TKLSIPTDSIWVPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFP 165

Query: 186 FDQQNCTLTFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKL 242  
 FD QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ +  
 Sbjct: 166 FDVQNCSTLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREF 221

Query: 243 S-RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 301  
 S N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLL  
 Sbjct: 222 SMESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNSGERVSFKITLL 281

Query: 302 LGYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLP 359  
 LGY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P  
 Sbjct: 282 LGYSVFLIIVSDTLPATAIGTPLIGVYFVVCMLLVISLAETIFIVRLVHKQDLQ-QPVP 340

Query: 360 RWLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEV 402  
 WL L+L + C P A + K G +H+ G K P  
 Sbjct: 341 AWLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGGPQDFEKS PRD 400



Query: 403 SAGQMPGPAAEALT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLF 457  
 P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL  
 Sbjct: 401 RCSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLA 460

Query: 458 MASSIITVICLWN 470  
 + + IT++ LW+  
 Sbjct: 461 VLAYSITLVMLWS 473

[>gi|30585371|gb|AAP36958.1| Homo sapiens 5-hydroxytryptamine (serotonin) recept  
 construct]  
 Length = 485

Score = 291 bits (744), Expect = 3e-77  
 Identities = 169/433 (39%), Positives = 254/433 (58%), Gaps = 33/433 (7%)

Query: 66 RKPFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGI 125  
 RK RPV + PT V+I + AIL+V+E+ +L++++W W + F+ WNPE+ + I  
 Sbjct: 52 RKGVRPVRDWRKPTTVSIDVIVYAILNVDEKNQVLTYYIWRQYWTDEFLQWNPEDFDNI 111

Query: 126 TKMSMAAKNLWLPDIFIIEIEMDVKTPKGLTAYVSNRIRYKKPMKVDSICNLDFYFP 185  
 TK+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FP  
 Sbjct: 112 TKLSIPTDSIWWPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFP 171

Query: 186 FDQQNCTLTFSSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKL 242  
 FD QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ +  
 Sbjct: 172 FDVQNCSLTFTSWLHTIQ----DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPYFREF 227

Query: 243 S-RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 301  
 S N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLL  
 Sbjct: 228 SMESSNYAEMKFYVIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNPSGERVSFKITLL 287

Query: 302 LGYNVFLLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLETFIFITHLLHVATTQPPPLP 359  
 LGY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P  
 Sbjct: 288 LGYSVFLIIVSDTLPTAIGTPLIGVYFVVMALLVISLAETIFIVRLVHKQDLQ-QPVP 346

Query: 360 RWLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV-----KEPEV 402  
 WL L+L + C P A + K G +H+ G K P  
 Sbjct: 347 AWLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGPPQDFEKSPRD 406

Query: 403 SAGQMPGPAAEALT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLF 457  
 P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL  
 Sbjct: 407 RCSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLA 466

Query: 458 MASSIITVICLWN 470  
 + + IT++ LW+  
 Sbjct: 467 VLAYSITLVMLWS 479

[>gi|1586341|prf||2203408A serotonin 3AS receptor  
 Length = 478

Score = 290 bits (742), Expect = 5e-77  
 Identities = 169/432 (39%), Positives = 253/432 (58%), Gaps = 33/432 (7%)

Query: 67 KPFPRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGIT 126  
 K RPV + PT V+I + AIL+V+E+ +L++++W W + F+ WNPE+ + IT

Sbjct: 47 KGVPRVDRWRKPTTVSIDVIVYAILNVDEKNQVLTTYIWYRQYWTDEFLQWNPEDFDNIT 106

Query: 127 KMSMAAKNLWLPDIFIIEIEMDVDPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFPF 186  
K+S+ ++W+PDI I E +DV K+P Y+ ++G ++ KP++V + C+LDI+ FPF

Sbjct: 107 KLSIPTDSIWVPDILINEFVDVGKSPNIPYVYIRHQGEVQNYKPLQVVTACSLDIYNFPF 166

Query: 187 DQQNCTLTFFSFLYTVDSMLLDMEKEVWEITD---ASRNILQTHGEWELLGLSKATAKLS 243  
D QNC+LTF+S+L+T+ D+ +W + + + R++ GEWELLG+ + S

Sbjct: 167 DVQNCSLTFTSWLHTIQ---DINISLWRLPEKVKSDRSVFMNQGEWELLGVLPHYFREFS 222

Query: 244 -RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLL 302  
N Y ++ FYV IRRRP YV++LL+PS FL+ +D + FYLP SG RV FKITLLL

Sbjct: 223 MESSNYAEMKFYVVIIRRRPLFYVVSLLLPSIFLMVMDIVGFYLPNSGERVSFKITLLL 282

Query: 303 GYNVFLMMSDLLPTS--GTPLIGVYFALCLSLMVGSLLLETIFITHLLHVATTQPPPLPR 360  
GY+VFL+++SD LP + GTPLIGVYF +C++L+V SL ETIFI L+H Q P+P

Sbjct: 283 GYSVFLIIIVSDTLPATAGTPLIGVYFVVCMAALLVISLTETIFIVRLVHKQDLQ-QPVPA 341

Query: 361 WLHSLLLHCNSPGRCC-----PTAPQKENK-----GPGLTPTHLPGV----KEPEVS 403  
WL L+L + C P A + K G TH+ G K P

Sbjct: 342 WLRHLVLERIAWLLCLREQSTSQRPPATSQATKTDDCSAMGNHCTHMGGPQDFEKS PRDR 401

Query: 404 AGQMPGPAEAEILT--GGSEWTRAQREHEAQKQHSVEL---WLQFSHAMDAMLFRLYLLFM 458  
P P EA L G + + R+ ++ E+ WL+ +D +LF +YLL +

Sbjct: 402 CSPPPPPREASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLAV 461

Query: 459 ASSIITVICLWN 470  
+ IT++ LW+

Sbjct: 462 LAYSITLVMLWS 473

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
Posted date: Dec 29, 2003 2:09 AM  
Number of letters in database: 519,349,222  
Number of sequences in database: 1,585,607

Lambda	K	H
0.323	0.138	0.429

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 50,992,532  
Number of Sequences: 1585607  
Number of extensions: 2252786  
Number of successful extensions: 5073  
Number of sequences better than 10.0: 97  
Number of HSP's better than 10.0 without gapping: 76  
Number of HSP's successfully gapped in prelim test: 21

Number of HSP's that attempted gapping in prelim test: 4817  
 Number of HSP's gapped (non-prelim): 103  
 length of query: 471  
 length of database: 519,349,222  
 effective HSP length: 128  
 effective length of query: 343  
 effective length of database: 316,391,526  
 effective search space: 108522293418  
 effective search space used: 108522293418  
 T: 11  
 A: 40  
 X1: 16 ( 7.5 bits)  
 X2: 38 (14.6 bits)  
 X3: 64 (24.7 bits)  
 S1: 41 (22.0 bits)  
 S2: 75 (33.5 bits)